

## SEQUENCE LISTING

<110> CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS  
<110> BIONOSTRA, S.L.

<120> EMPTY CAPSIDS (VLPs(-VP4)) OF THE INFECTIOUS BURSAL DISEASE VIRUS (IBDV), OBTAINMENT PROCESS AND APPLICATIONS

<130> P1392PC

<150> ES P200400121  
<151> 2004-01-21 (January 21, 2004)

<160> 10  
<170> PatentIn version 3.1

<210> 1  
<211> 35  
<212> DNA  
<213> Artificial sequence

<220> Synthetic DNA  
<223> Oligo I primer

<400> 1  
gcgcagatct atgacaaacc tgtcagatca aaccc 35

<210> 2  
<211> 34  
<212> DNA  
<213> Artificial sequence

<220> Synthetic DNA  
<223> Oligo II primer

<400> 2  
gcgcaagctt aggcgagagt cagctgcctt atgc 34

<210> 3  
<211> 7595  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Plasmid pFBD/pVP2-his-VP3

<221> promoter  
<222> (157)..(285)  
<223> Promotor ppolh

<221> CDS  
<222> (291)..(1289)  
<223> pVP2 ORF

&lt;221&gt; promoter

&lt;222&gt; (7443)..(7503)

&lt;223&gt; Promoter p10

&lt;400&gt; 3

gggtgatcaa gtcttcgtcgc agtgattgta aataaaatgt aatttacagt atagtatttt 60

aattaatata caaatgattt gataataatt cttattttaac tataatatat tgtgttgggt 120

tgaattaaag gtccgtatac tccggaatat taatagatca tggagataat taaaatgata 180

accatctcgc aaataaataa gtatttttact gtttttcgtaa cagtttttgta ataaaaaaac 240

ctataaatat tccggattat tcataccgtc ccaccatcgg gcgcggatct atg aca 296  
Met Thr  
1aac ctg tca gat caa acc cag cag att gtt ccg ttc ata cgg agc ctt 344  
Asn Leu Ser Asp Gln Thr Gln Gln Ile Val Pro Phe Ile Arg Ser Leu  
5 10 15ctg atg cca aca acc gga ccg gcg tcc att ccg gac gac acc ctg gag 392  
Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr Leu Glu  
20 25 30aag cac act ctc agg tca gag acc tcg acc tac aat ttg act gtg ggg 440  
Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr Val Gly  
35 40 45 50gac aca ggg tca ggg cta att gtc ttt ttc cct gga ttc cct ggc tca 488  
Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro Gly Phe Pro Gly Ser  
55 60 65att gtg ggt gct cac tac aca ctg cag ggc aat ggg aac tac aag ttc 536  
Ile Val Gly Ala His Tyr Thr Leu Gln Gly Asn Gly Asn Tyr Lys Phe  
70 75 80gat cag atg ctc ctg act gcc cag aac cta ccg gcc agt tac aac tac 584  
Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro Ala Ser Tyr Asn Tyr  
85 90 95tgc agg cta gtg agt cgg agt ctc aca gtg agg tca agc aca ctt cct 632  
Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg Ser Ser Thr Leu Pro  
100 105 110ggt ggc gtt tat gca cta aac ggc acc ata aac gcc gtg acc ttc caa 680  
Gly Gly Val Tyr Ala Leu Asn Gly Thr Ile Asn Ala Val Thr Phe Gln  
115 120 125 130gga agc ctg agt gaa ctg aca gat gtt agc tac aat ggg ttg atg tct 728  
Gly Ser Leu Ser Glu Leu Thr Asp Val Ser Tyr Asn Gly Leu Met Ser  
135 140 145gca aca gcc aac atc aac gac aaa att ggg aac gtc cta gta ggg gaa 776  
Ala Thr Ala Asn Ile Asn Asp Lys Ile Gly Asn Val Leu Val Gly Glu  
150 155 160ggg gtc acc gtc ctc agc tta ccc aca tca tat gat ctt ggg tat gtg 824  
Gly Val Thr Val Leu Ser Leu Pro Thr Ser Tyr Asp Leu Gly Tyr Val  
165 170 175

agg ctt ggt gac ccc att ccc gca ata ggg ctt gac cca aaa atg gta	872
Arg Leu Gly Asp Pro Ile Pro Ala Ile Gly Leu Asp Pro Lys Met Val	
180 185 190	
gcc aca tgt gac agc agt gac agg ccc aga gtc tac acc ata act gca	920
Ala Thr Cys Asp Ser Ser Asp Arg Pro Arg Val Tyr Thr Ile Thr Ala	
195 200 205 210	
gcc gat gat tac caa ttc tca tca cag tac caa cca ggt ggg gta aca	968
Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Pro Gly Gly Val Thr	
215 220 225	
atc aca ctg ttc tca gcc aac att gat gcc atc aca agc ctc agc gtt	1016
Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser Val	
230 235 240	
ggg gga gag ctc gtg ttt cga aca agc gtc cac ggc ctt gta ctg ggc	1064
Gly Gly Glu Leu Val Phe Arg Thr Ser Val His Gly Leu Val Leu Gly	
245 250 255	
gcc acc atc tac ctc ata ggc ttt gat ggg aca acg gta atc acc agg	1112
Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Thr Val Ile Thr Arg	
260 265 270	
gct gtg gcc gca aac aat ggg ctg acg acc ggc acc gac aac ctt atg	1160
Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu Met	
275 280 285 290	
cca ttc aat ctt gtg att cca aca aac gag ata acc cag cca atc aca	1208
Pro Phe Asn Leu Val Ile Pro Thr Asn Glu Ile Thr Gln Pro Ile Thr	
295 300 305	
tcc atc aaa ctg gag ata gtg acc tcc aaa agt ggt ggt cag gca ggg	1256
Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala Gly	
310 315 320	
gat cag atg tca tgg tcg gca aga ggg agc cta gcagtgcga tccatggtgg	1309
Asp Gln Met Ser Trp Ser Ala Arg Gly Ser Leu	
325 330	
caactatcca ggggccctcc gtcccgtcac gctagtggcc tacgaaagag tggcaacagg	1369
atccgtcggtt acggtcgctg gggtgagcaa cttcgagctg atoccaaata ctgaactagc	1429
aaagaacctg gttacagaat acggccgatt tgaccagga gccatgaact acacaaaatt	1489
gatactgagt gagagggacc gtcttggcat caagaccgtc tggccaacaa gggagtacac	1549
tgactttcgt gaatacttca tggaggtggc cgacctcaac tctcccctga agattgcagg	1609
agcattcggc ttcaaagaca taatccgggc cataaggagg atagctgtgc cggtggtctc	1669
cacattgttc ccacctgccg ctcccctagc ccatgcaatt ggggaagggtg tagactacct	1729
gctgggcat gagggccagg ccgcttcagg aactgctcga gccgcgtcag gaaaagcaag	1789
agctgcctca ggccgcataa ggcagctgac tctcgccctaa gcttgtcgag aagtactaga	1849
ggatcataat cagccatacc acattttagt aggttttact tgcttttaaaa aacctccac	1909

acctccccct	gaacctgaaa	cataaaatga	atgcaattgt	tgttgttaac	ttgtttattg	1969
cagcttataa	tggttacaaa	taaagcaata	gcatcacaaa	tttcacaaat	aaagcatttt	2029
tttcactgca	ttctagttgt	ggtttgtcca	aactcatcaa	tgtatcttat	catgtctgga	2089
tctgatcact	gcttgagcct	aggagatccg	aaccagataa	gtgaaatcta	gttccaaact	2149
attttgtcat	ttttaatttt	cgtattagct	tacgacgcta	caccagttc	ccatctattt	2209
tgtcactctt	ccctaaataa	tccttaaaaa	ctccatttcc	accctccca	gttcccaact	2269
attttgtccg	cccacagcgg	ggcatttttc	ttcctgttat	gtttttaatc	aaacatcctg	2329
ccaactccat	gtgacaaacc	gtcatcttcg	gctacttttt	ctctgtcaca	gaatgaaaat	2389
ttttctgtca	tctcttcggt	attaatgttt	gtaattgact	gaatatcaac	gcttatattgc	2449
agcctgaatg	gcgaatggga	cgcgccctgt	agcggcgcat	taagcgcggc	gggtgtgggtg	2509
gttacgcgca	gcgtgaccgc	tacacttgcc	agcgccctag	cgcccgcctc	tttcgccttc	2569
ttcccttcct	ttctcgccac	gttcgcccgc	tttccccgtc	aagctctaaa	tcgggggctc	2629
cctttagggg	tcgatttag	tgctttacgg	cacctcgacc	ccaaaaaact	tgattagggg	2689
gatggttcac	gtagtgggcc	atcgccctga	tagacggttt	ttcgcccttt	gacgttggag	2749
tccacgttct	ttaatagtgg	actcttgttc	caaactggaa	caacactcaa	ccctatctcg	2809
gtctattctt	ttgatttata	agggattttg	ccgatttcgg	cctattgggt	aaaaaatgag	2869
ctgattttaac	aaaaatttaa	cgcgaaat	aacaaaatat	taacgtttac	aatttcaggt	2929
ggcacttttc	ggggaaatgt	gcgcggaacc	cctatttggt	tatTTTTtcta	aatacattca	2989
aatatgtatc	cgctcatgag	acaataaccc	tgataaatgc	ttcaataata	ttgaaaaagg	3049
aagagtatga	gtattcaaca	tttccgtgtc	gcccttattc	cctTTTTttgc	ggcattttgc	3109
cttcctgttt	ttgctcacc	agaaacgctg	gtgaaagtaa	aagatgctga	agatcagttg	3169
gggtgcacgag	tgggttacat	cgaactggat	ctcaacagcg	gtaagatcct	tgagagtttt	3229
cgccccgaag	aacgttttcc	aatgatgagc	actttttaag	ttctgctatg	tggcgcggtg	3289
ttatcccgta	ttgacgcggg	gcaagagcaa	ctcggtcgcc	gcatacacta	ttctcagaat	3349
gacttggttg	agtactcacc	agtcacagaa	aagcatctta	cggatggcat	gacagtaaga	3409
gaattatgca	gtgctgccat	aaccatgagt	gataacactg	cggccaactt	acttctgaca	3469
acgatcggag	gaccgaagga	gctaaccgct	tttttgcaca	acatggggga	tcatgtaact	3529
cgccttgatc	gttggggaacc	ggagctgaat	gaagccatac	caaacgacga	gcgtgacacc	3589
acgatgcctg	tagcaatggc	aacaacgttg	cgcaaactat	taactggcga	actacttact	3649
ctagcttccc	ggcaacaatt	aatagactgg	atggaggcgg	ataaagttgc	aggaccactt	3709

ctgcgctcgg	cccttccggc	tggctggttt	attgctgata	aatctggagc	cggtgagcgt	3769
gggtctcgcg	gtatcattgc	agcactgggg	ccagatggta	agccctcccg	tatcgtagtt	3829
atctacacga	cggggagtca	ggcaactatg	gatgaacgaa	atagacagat	cgctgagata	3889
gggtgcctcac	tgattaagca	ttggtaactg	tcagaccaag	tttactcata	tatacttttag	3949
attgatttaa	aacttcattt	ttaatttaaa	aggatctagg	tgaagatcct	ttttgataat	4009
ctcatgacca	aatccctta	acgtgagttt	tcgttccact	gagcgtcaga	ccccgtagaa	4069
aagatcaaag	gatcttcttg	agatcctttt	tttctgcgcg	taatctgctg	cttgcaaaca	4129
aaaaaaccac	cgctaccagc	ggtggtttgt	ttgccggatc	aagagctacc	aactcttttt	4189
ccgaaggtaa	ctggcttcag	cagagcgcag	ataccaaata	ctgtccttct	agtgtagccg	4249
tagttaggcc	accacttcaa	gaactctgta	gcaccgccta	catacctcgc	tctgctaata	4309
ctgttaccag	tggctgctgc	cagtggcgat	aagtcgtgtc	ttaccggggt	ggactcaaga	4369
cgatagttac	cggataaggc	gcagcggtcg	ggctgaacgg	ggggttcgtg	cacacagccc	4429
agcttggagc	gaacgaccta	caccgaactg	agatacctac	agcgtgagca	ttgagaaagc	4489
gccacgcttc	ccgaagggag	aaaggcggac	aggtatccgg	taagcggcag	ggtcggaaca	4549
ggagagcgca	cgagggagct	tccaggggga	aacgcctggg	atcttttatag	tcctgtcggg	4609
tttcgccacc	tctgacttga	gcgtcgattt	ttgtgatgct	cgtcaggggg	gcggagccta	4669
tggaaaaacg	ccagcaacgc	ggccttttta	cggttcctgg	cctttttgctg	gccttttgct	4729
cacatgttct	ttcctgcgtt	atcccctgat	tctgtggata	accgtattac	cgcctttgag	4789
tgagctgata	ccgctcgccg	cagccgaacg	accgagcgca	gcgagtcagt	gagcgaggaa	4849
gcggaagagc	gcctgatgcg	gtatttttctc	cttacgcata	tgtgcggtat	ttcacaccgc	4909
agaccagccg	cgtaacctgg	caaaatcggg	tacggttgag	taataaatgg	atgccctgcg	4969
taagcgggtg	tgggcggaca	ataaagtctt	aaactgaaca	aatagatct	aaactatgac	5029
aataaagtct	taaactagac	agaatagttg	taaactgaaa	tcagtccagt	tatgctgtga	5089
aaaagcatac	tggacttttg	ttatggctaa	agcaaactct	tcattttctg	aagtgcaaat	5149
tgcccgtcgt	attaaagagg	ggcgtggcca	agggcatggg	aaagactata	ttcgcggcgt	5209
tgtgacaatt	taccgaacaa	ctccgcggcc	gggaagccga	tctcggcttg	aacgaattgt	5269
taggtggcgg	tacttgggtc	gatatcaaag	tgcatacatt	cttcccgtat	gcccactttt	5329
gtatagagag	ccactgcggg	atcgtcaccg	taatctgctt	gcacgtagat	cacataagca	5389
ccaagcgcgt	tggcctcatg	cttgaggaga	ttgatgagcg	cgggtggcaat	gccctgcctc	5449
cggtgctcgc	cggagactgc	gagatcatag	atatagatct	cactacgcgg	ctgctcaaac	5509

ctgggacagaa cgtaagccgc gagagcgcca acaaccgctt cttggtcgaa ggcagcaagc 5569  
gcgatgaatg tcttactacg gagcaagtcc ccgaggtaat cggagtccgg ctgatgttgg 5629  
gagtaggtgg ctacgtctcc gaactcacga ccgaaaagat caagagcagc ccgcatggat 5689  
ttgacttggg cagggccgag cctacatgtg cgaatgatgc ccatacttga gccacctaac 5749  
tttgttttag ggcgactgcc ctgctgcgta acatcggtgc tgctgcgtaa catcgttgct 5809  
gctccataac atcaaacatc gacccacggc gtaacgcgct tgctgcttgg atgcccagag 5869  
catagactgt acaaaaaaac agtcataaca agccatgaaa accgccactg cgccgttacc 5929  
accgctgcgt tcgggtcaagg ttctggacca gttgcgtgag cgcatacgct acttgcatta 5989  
cagtttacga accgaacagg cttatgtcaa ctgggttcgt gccttcatcc gtttccacgg 6049  
tgtgcgtcac ccggcaacct tgggcagcag cgaagtcgag gcatttctgt cctggctggc 6109  
gaacgagcgc aaggtttcgg tctccacgca tcgtcaggca ttggcggcct tgctgttctt 6169  
ctacggcaag gtgctgtgca cggatctgcc ctggcttcag gagatcggta gacctcggcc 6229  
gtcgcggcgc ttgccggtgg tgctgacccc ggatgaagtg gttcgcaccc tcggttttct 6289  
ggaaggcgag catcgtttgt tcgcccagga ctctagctat agttctagtg gttggcctac 6349  
gtacccgtag tggctatggc agggcttgcc gcccgcagct tggctgcgag ccctgggcct 6409  
tcacccgaac ttggggggtg ggggtgggaa aaggaagaaa cgcgggcgta ttggtcccaa 6469  
tggggtctcg gtggggtatc gacagagtgc cagccctggg accgaacccc gcgtttatga 6529  
acaaacgacc caacaccgct gcgttttatt ctgtcttttt attgccgtca tagcgcgggt 6589  
tccttcgggt attgtctcct tccgtgttcc agttagcctc ccccatctcc cggtagcgca 6649  
tgctcagaga ctgcaggctc tagattcgaa agcggccgcg actagtgagc tcgtcgacgt 6709  
aggcctttga attccggatc ctcaactcaag gtcctcatca gagacgggtc tgatccagcg 6769  
gccagccga ccaggggggtc tctgtgttgg agcattgggt tttggcttgg gctttggtag 6829  
agcccgcctg ggattgcgat gcttcatctc catcgcagtc aagagcagat ctttcatctg 6889  
ttcttgggtt gggccacgtc catggttgat ttcatagact ttggcaactt cgtctatgaa 6949  
agcttgggggt ggctctgcct gtcctggagc cccgtagatc gacgtagctg cccttaggat 7009  
ttgttcttct gatgccaacc ggctcttctc tgcatgcacg tagtctagat agtcctcggt 7069  
tgggtccggt atttctcggt tggtctgcca gtactttacc tggcctgggc ttggccctcg 7129  
gtgcccattg agtgctaccc attctgggtg tgcaaagtag atgcccattg tctccatctt 7189  
ctttgagatc cgtgtgtctt tttccctctg tgcttctctt ggtgtggggc cccgagcctc 7249  
cactcogtag cctgctgtcc cgtacttggc cctttgcgac ttgctgcctg cttgtgggtg 7309



gtttgcaaga aaatttcgca tccgatgggc gttcgggtcg ctgagtgcga agttggccat 7369  
 gtcagtcaca atccattct cttccagcca catgaacaca ctgagtgcag attggaatag 7429  
 tgggtccacg ttggctgctg cttccattgc tctgacggca ctctcgagtt cgggggtctc 7489  
 tttgaactct gatgcagcca tggcgccctg aaaatacagg ttttcggtcg ttgggatatc 7549  
 gtaatcgtga tggatgatgg gatggtagta cgacatgggt tcggac 7595

<210> 4  
 <211> 333  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> pVP2-his-VP3 protein

<400> 4  
 Met Thr Asn Leu Ser Asp Gln Thr Gln Gln Ile Val Pro Phe Ile Arg  
 1 5 10 15  
 Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr  
 20 25 30  
 Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr  
 35 40 45  
 Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro Gly Phe Pro  
 50 55 60  
 Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Gly Asn Gly Asn Tyr  
 65 70 75 80  
 Lys Phe Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro Ala Ser Tyr  
 85 90 95  
 Asn Tyr Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg Ser Ser Thr  
 100 105 110  
 Leu Pro Gly Gly Val Tyr Ala Leu Asn Gly Thr Ile Asn Ala Val Thr  
 115 120 125  
 Phe Gln Gly Ser Leu Ser Glu Leu Thr Asp Val Ser Tyr Asn Gly Leu  
 130 135 140  
 Met Ser Ala Thr Ala Asn Ile Asn Asp Lys Ile Gly Asn Val Leu Val  
 145 150 155 160  
 Gly Glu Gly Val Thr Val Leu Ser Leu Pro Thr Ser Tyr Asp Leu Gly  
 165 170 175  
 Tyr Val Arg Leu Gly Asp Pro Ile Pro Ala Ile Gly Leu Asp Pro Lys  
 180 185 190  
 Met Val Ala Thr Cys Asp Ser Ser Asp Arg Pro Arg Val Tyr Thr Ile  
 195 200 205

Thr Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Pro Gly Gly  
 210 215 220  
 Val Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu  
 225 230 235 240  
 Ser Val Gly Gly Glu Leu Val Phe Arg Thr Ser Val His Gly Leu Val  
 245 250 255  
 Leu Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Thr Val Ile  
 260 265 270  
 Thr Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn  
 275 280 285  
 Leu Met Pro Phe Asn Leu Val Ile Pro Thr Asn Glu Ile Thr Gln Pro  
 290 295 300  
 Ile Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln  
 305 310 315 320  
 Ala Gly Asp Gln Met Ser Trp Ser Ala Arg Gly Ser Leu  
 325 330

<210> 5  
 <211> 35  
 <212> DNA  
 <213> Artificial sequence

<220> Synthetic DNA  
 <223> Oligo III primer

<400> 5  
 gcgcagatct atgacaaacc tgtcagatca aaccc

35

<210> 6  
 <211> 34  
 <212> DNA  
 <213> Artificial sequence

<220> Synthetic DNA  
 <223> Oligo IV primer

<400> 6  
 gcgcaagctt aggcgagagt cagctgcctt atgc

34

<210> 7  
 <211> 33  
 <212> DNA  
 <213> Artificial sequence

<220> Synthetic DNA  
 <223> Oligo V primer

<400> 7  
 gcgcgaattc gatggcatca gagttcaaag aga

33



<210> 8  
 <211> 32  
 <212> DNA  
 <213> Artificial sequence

<220> Synthetic DNA  
 <223> Oligo VI primer

<400> 8  
 cgcggtatccc tcaaggctcct catcagagac gg 32

<210> 9  
 <211> 9600  
 <212> DNA  
 <213> Artificial sequence

<223> Plasmid pESCURA/pVP2-VP3-GFP

<221> promoter  
 <222> (5649)..(5859)  
 <223> Promoter GAL 1 (pVP2)

<221> promoter  
 <222> (7402)..(8080)  
 <223> Promoter GAL 2 (VP3-GFP)

<221> CDS  
 <222> (8086)..(9597)  
 <223> VP3-GFP ORF

<400> 9  
 ggccgcacta gtatcgatgg attacaagga tgacgacgat aagatctgag ctcttaatta 60  
 acaattcttc gccagagggtt tgggtcaagtc tccaatcaag gttgtcggct tgtctacctt 120  
 gccagaaatt tacgaaaaga tggaaaaggg tcaaatacgtt ggtagatacg ttgttgacac 180  
 ttctaaataa gcgaatttct tatgatttat gatTTTTtatt attaaataag ttataaaaaa 240  
 aataagtgtg tacaaatttt aaagtgactc ttaggtttta aaacgaaaat tcttattctt 300  
 gagtaactct ttcctgtagg tcagggttgct ttctcaggta tagcatgagg tcgctccaat 360  
 tcagctgcat taatgaatcg gccaacgcgc ggggagaggc ggtttgcgta ttgggcgctc 420  
 ttccgcttcc tcgctcactg actcgctgcg ctcggtcgtt cggctgcggc gagcggatatc 480  
 agctcactca aaggcggtaa tacggttatc cacagaatca ggggataacg caggaaagaa 540  
 catgtgagca aaaggccagc aaaaggccag gaaccgtaaa aaggccgcgt tgctggcggtt 600  
 tttccatagg ctccgcccc ctgacgagca tcacaaaaat cgacgctcaa gtcagagggtg 660  
 gcgaaacccg acaggactat aaagatacca ggcgtttccc cctggaagct ccctcgctgcg 720  
 ctctcctggt ccgaccctgc cgcttaccgg atacctgtcc gcctttctcc cttcgggaag 780  
 cgtggcgctt tctcatagct cacgctgtag gtatctcagt tcggtgtagg tcgttcgctc 840

caagctgggc tgtgtgcacg aaccccccggt tcagcccgac cgctgcgcct tatccggtaa 900  
ctatcgtcctt gagtccaacc cggtaagaca cgacttatcg ccactggcag cagccactgg 960  
taacaggatt agcagagcga ggtatgtagg cgggtgctaca gagttcttga agtgggtggcc 1020  
taactacggc tacactagaa ggacagtatt tggatatctgc gctctgctga agccagttac 1080  
cttcggaaaa agagttggta gctcttgatc cggcaaacaa accaccgctg gtagcgggtgg 1140  
ttttttttggt tgcaagcagc agattacgcg cagaaaaaaaa ggatctcaag aagatccttt 1200  
gatcttttctt acgggggtctg acgctcagtg gaacgaaaac tcacgttaag ggatttttggt 1260  
catgagatta tcaaaaagga tcttcaccta gatcctttta aattaaaaat gaagttttta 1320  
atcaatctaa agtatatatg agtaaacttg gtctgacagt taccaatgct taatcagtga 1380  
ggcacctatc tcagcgatct gtctatttcg ttcattccata gttgcctgac tccccgtcgt 1440  
gtagataact acgatacggg agggccttacc atctggcccc agtgctgcaa tgataccgcg 1500  
agaccacgc tcaccggctc cagatttatc agcaataaac cagccagccg gaagggccga 1560  
gcgcagaagt ggtcctgcaa ctttatccgc ctccatccag tctattaatt gttgccggga 1620  
agctagagta agtagttcgc cagttaatag tttgcgcaac gttgttgcca ttgctacagg 1680  
catcgtgggtg tcacgctcgt cgtttgggtat ggcttcattc agctccggtt cccaacgatc 1740  
aaggcgagtt acatgatccc ccatgttggtg caaaaaagcg gttagctcct tcggtcctcc 1800  
gatcgttggtc agaagtaagt tggccgcagt gttatcactc atggttatgg cagcactgca 1860  
taattctctt actgtcatgc catccgtaag atgcttttct gtgactgggtg agtactcaac 1920  
caagtcattc tgagaatagt gtatgcggcg accgagttgc tcttgcccgg cgtcaatacg 1980  
ggataatacc gcgccacata gcagaacttt aaaagtgctc atcattggaa aacgttcttc 2040  
ggggcgaaaa ctctcaagga tcttaccgct gttgagatcc agttcgatgt aaccactcgt 2100  
tgcacccaac tgatcttcag catctttttac tttcaccagc gtttctgggt gagcaaaaac 2160  
aggaaggcaa aatgccgcaa aaaagggaat aagggcgaca cggaaatgtt gaatactcat 2220  
actcttcctt tttcaatatt attgaagcat ttatcagggt tattgtctca tgagcggata 2280  
catatttgaa tgtattttaga aaaataaaca aataggggtt ccgcgcacat ttccccgaaa 2340  
agtgccacct gaacgaagca tctgtgcttc atttttaga acaaaaatgc aacgcgagag 2400  
cgctaatttt tcaaacaag aatctgagct gcattttttac agaacagaaa tgcaacgcga 2460  
aagcgctatt ttaccaacga agaactctgtg cttcatTTTT gtaaaacaaa aatgcaacgc 2520  
gagagcgcta atttttcaaa caaagaatct gagctgcatt ttacagaac agaaatgcaa 2580  
cgcgagagcg ctatttttacc aacaagaat ctatacttct tttttgttct acaaaaatgc 2640

atcccgagag cgctatTTTT ctaacaaagc atcttagatt actTTTTTtc tcctttgtgc 2700  
gctctataat<sup>h</sup>gcagtcctt gataactttt tgcactgtag gtccgttaag gttagaagaa 2760  
ggctactttg gtgtctatTT tctcttccat aaaaaaagcc tgactccact tcccgcgttt 2820  
actgattact agcgaagctg cgggtgcatt ttttcaagat aaaggcatcc ccgattatat 2880  
tctataccga tgtggattgc gcatactttg tgaacagaaa gtgatagcgt tgatgattct 2940  
tcattggtca gaaaattatg aacggtttct tctatTTTgt ctctatatac tacgtatagg 3000  
aaatgtttac attttcgtat tgttttcgat tcaactctatg aatagtTctt actacaattt 3060  
ttttgtctaa agagtaatac tagagataaa cataaaaaat gtagaggTcg agtttagatg 3120  
caagttcaag gagcgaaagg tggatgggta ggTtatatag ggatatagca cagagatata 3180  
tagcaaagag atactTTTga gcaatgtttg tggaagcggT attcgcaata ttttagtagc 3240  
tcgttacagt ccggTgcgtt tttggTTTTt tgaaagtgcg tcttcagagc gctTTTTggtt 3300  
ttcaaaagcg ctctgaagtt cctatacttt ctagagaata ggaactTcg aataggaact 3360  
tcaaagcgtt tccgaaaacg agcgctTccg aaaatgcaac gcgagctgcg cacatacagc 3420  
tcaactgttca cgtcgcacct atatctgcgt gttgcctgta tatatatata catgagaaga 3480  
acggcatagt gcgtgtttat gcttaaattgc gtacttatat gcgtctatTT atgtaggatg 3540  
aaaggtagtc tagtacctcc tgtgatatta tcccatTcca tgcgggggtat cgtatgcttc 3600  
cttcagcact accctTTtagc tgttctatat gctgccactc ctcaattgga ttagtctcat 3660  
ccttcaatgc tatcatTTcc tttgatattg gatcatacta agaaaccatt attatcatga 3720  
cattaaccta taaaaatagg cgtatcacga ggccctTtcg tctcgcgcgT ttcggTgatg 3780  
acggTgaaaa cctctgacac atgcagctcc cggagacggT cacagctTgt ctgtaagcgg 3840  
atgccgggag cagacaagcc cgtcagggcg cgtcagcggg tgttggcggg tgcgggggct 3900  
ggcttaacta tgcggcatca gagcagattg tactgagagt gcaccatacc acagctTTTc 3960  
aattcaattc atcatTTTTt ttttattctt ttttttgatt tcggTttctt tgaaattTTTT 4020  
ttgattcggt aatctccgaa cagaaggaag aacgaaggaa ggagcacaga cttagattgg 4080  
tatatatacg catatgtagt gttgaagaaa catgaaattg ccagtatTc ttaacccaac 4140  
tgcacagAAC aaaaacctgc aggaaacgaa gataaatcat gtcgaaagct acatataagg 4200  
aacgtgctgc tactcatcct agtcctgttg ctgccagct atttaatatc atgcacgaaa 4260  
agcaaacaaa cttgtgtgct tcattggatg ttcgtaccac caaggaatta ctggagttag 4320  
ttgaagcatt aggtcccaaa atttgtttac taaaaacaca tgtggatatc ttgactgatt 4380  
tttccatgga gggcacagtt aagccgctaa aggcattatc cgccaagtac aattTTTTtac 4440

tcttogaaga cagaaaatth gctgacattg gtaatacagt caaattgcag tactctgcgg 4500  
gtgtatacag aatagcagaa tgggcagaca ttacgaatgc acacggtgtg gtgggccag 4560  
gtattgttag cggtttgaag caggcggcag aagaagtaac aaaggaacct agaggccttt 4620  
tgatgttagc agaattgtca tgcaagggct ccctatctac tggagaatat actaagggtg 4680  
ctgttgacat tgcgaagagc gacaaagatt ttgttatcgg ctttattgct caaagagaca 4740  
tgggtggaag agatgaaggt tacgattggt tgattatgac acccggtgtg ggtttagatg 4800  
acaagggaga cgcattgggt caacagtata gaaccgtgga tgatgtggtc tctacaggat 4860  
ctgacattat tattgttgga agaggactat ttgcaaaggg aagggatgct aaggtagagg 4920  
gtgaacgtta cagaaaagca ggctgggaag catatttgag aagatgcggc cagcaaaact 4980  
aaaaaactgt attataagta aatgcatgta tactaaactc acaaattaga gcttcaatth 5040  
aattatatca gttattacc c tatgcggtgt gaaataccgc acagatgcgt aaggagaaaa 5100  
taccgcatca ggaaattgta aacgttaata ttttgttaaa attcgcgtta aatttttgtt 5160  
aatcagctc attttttaac caataggccg aaatcggcaa aatcccttat aaatcaaaag 5220  
aatagaccga gatagggttg agtggtgttc cagtttgga caagagtcca ctattaaaga 5280  
acgtggactc caacgtcaaa gggcgaaaaa ccgtctatca gggcgatggc ccactacgtg 5340  
aaccatcacc ctaatcaagt tttttgggggt cgagggtgccg taaagcacta aatcggaacc 5400  
ctaaagggag ccccgatth agagcttgac ggggaaagcc ggcgaacgtg gcgagaaagg 5460  
aagggaagaa agcgaaagga gcgggcgcta gggcgctggc aagtgtagcg gtcacgctgc 5520  
gcgtaaccac cacacccgcc gcgcttaatg cgccgctaca gggcgcgctc cgccattcgc 5580  
cattcaggct gcgcaactgt tgggaagggc gatcggtgcg ggcctcttcg ctattacgcc 5640  
agctggatct tcgagcgtcc caaaaccttc tcaagcaagg ttttcagtat aatgttacat 5700  
gcgtacacgc gtctgtacag aaaaaaaga aaaatttgaa atataaataa cgttcttaat 5760  
actaacataa ctataaaaaa ataaataggg acctagactt caggttgtct aactccttcc 5820  
ttttcggtta gagcggatct tagctagccg cggtaccaag cttaggcgag agtcagctgc 5880  
cttatgcggc ctgaggcagc tcttgcttht cctgacgcgg ctcgagcagt tcctgaagcg 5940  
gcctgggcct catcgcccag caggtagtct acaccttccc caattgcatg ggctagggga 6000  
gcggcagggtg ggaacaatgt ggagaccacc ggcacagcta tcctccttat ggcccggtt 6060  
atgtctthga agccgaatgc tctgcaatc ttcaggggag agttgaggtc ggccacctcc 6120  
atgaagtatt cacgaaagtc agtgtactcc cttgttggcc agacggtctt gatgccaaga 6180  
, cggtccctct cactcagtat caattthgtg tagttcatgg ctctgggtc aaatcggccg 6240

tattctgtaa ccaggttctt tgctagttca ggatttggga tcagctcgaa gttgctcacc 6300  
ccagcgaccg taacgacgga tcctgttgcc actctttcgt aggccactag cgtgacggga 6360  
cggagggccc ctggatagtt gccaccatgg atcgtcactg ctaggctccc tcttgccgac 6420  
catgacatct gatcccctgc ctgaccacca cttttggagg tcactatctc cagtttgatg 6480  
gatgtgattg gctgggttat ctcgtttgtt ggaatcacia gattgaatgg cataaggttg 6540  
tcggtgccgg tcgtcagccc attgtttgcg gccacagccc tgggtgattac cgttgtccca 6600  
tcaaagccta tgaggtagat ggtggcgccc agtacaaggc cgtggacgct tgttcgaaac 6660  
acgagctctc cccaacgct gaggcttggt atggcatcaa tgttggctga gaacagtgtg 6720  
attgttacct cacctgggtg gtactgtgat gagaattggg aatcatcggc tgcagttatg 6780  
gtgtagactc tgggcctgtc actgctgtca catgtggcta ccatttttgg gtcaagccct 6840  
attgcgggaa tggggtcacc aagcctcaca taccacagat catatgatgt gggtaagctg 6900  
aggacggtga ccccttcccc tactaggacg ttcccaattt tgtcgttgat gttggctgtt 6960  
gcagacatca acccattgta gctaacatct gtcagttcac tcaggcttcc ttggaaggtc 7020  
acggcgttta tgggtgccgtt tagtgcataa acgccaccag gaagtgtgct tgacctcact 7080  
gtgagactcc gactcactag cctgcagtag ttgtaactgg ccggtagggt ctgggcagtc 7140  
aggagcatct gatcgaactt gtagttccca ttgccctgca gtgtgtagtg agcaccacaca 7200  
attgagccag ggaatccagg gaaaaagaca attagccctg accctgtgtc cccacagtc 7260  
aaattgtagg tcgaggtctc tgacctgaga gtgtgcttct ccagggtgtc gtccggaatg 7320  
gacgccggtc cggttgttgg catcagaagg ctccgtatga acggaacaat ctgctgggtt 7380  
tgatctgaca ggtttgtcat agatccgggg ttttttctcc ttgacgttaa agtatagagg 7440  
tatattaaca attttttgtt gatactttta ttacatttga ataagaagta atacaaaccg 7500  
aaaatgttga aagtattagt taaagtgggt atgcagtttt tgcatttata tatctgttaa 7560  
tagatcaaaa atcatcgctt cgctgattaa ttaccccaga aataaggcta aaaaactaat 7620  
cgcatatca tcctatgggt gttaatttga ttcgttcatt tgaaggtttg tggggccagg 7680  
ttactgcaa tttttcctct tcataaccat aaaagctagt attgtagaat ctttattgtt 7740  
cggagcagtg cggcgcgagg cacatctgcg tttcaggaac gcgaccggtg aagacgagga 7800  
cgcacggagg agagtcttcc ttoggagggc tgtcaccgcg tcggcggtt ctaatccgta 7860  
cttcaatata gcaatgagca gttaagcgta ttactgaaag ttccaaagag aaggtttttt 7920  
taggctaaga taatggggct ctttacattt ccacaacata taagtaagat tagatatgga 7980  
tatgtatatg gatatgtata tgggtggtaat gccatgtaat atgattatta aacttctttg 8040



cgtccatcca aaaaaaaagt aagaattttt gaaaattcga attcg atg gct gca tca															8097
Met Ala Ala Ser															
1															
gag ttc aaa gag acc ccc gaa ctc gag agt gcc gtc aga gca atg gaa															8145
Glu Phe Lys Glu Thr Pro Glu Leu Glu Ser Ala Val Arg Ala Met Glu															
5 10 15 20															
gca gca gcc aac gtg gac cca cta ttc caa tct gca ctc agt gtg ttc															8193
Ala Ala Ala Asn Val Asp Pro Leu Phe Gln Ser Ala Leu Ser Val Phe															
25 30 35															
atg tgg ctg gaa gag aat ggg att gtg act gac atg gcc aac ttc gca															8241
Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp Met Ala Asn Phe Ala															
40 45 50															
ctc agc gac ccg aac gcc cat cgg atg cga aat ttt ctt gca aac gca															8289
Leu Ser Asp Pro Asn Ala His Arg Met Arg Asn Phe Leu Ala Asn Ala															
55 60 65															
cca caa gca ggc agc aag tcg caa agg gcc aag tac ggg aca gca ggc															8337
Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys Tyr Gly Thr Ala Gly															
70 75 80															
tac gga gtg gag gct cgg ggc ccc aca cca gag gaa gca cag agg gaa															8385
Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu Glu Ala Gln Arg Glu															
85 90 95 100															
aaa gac aca cgg atc tca aag aag atg gag acc atg ggc atc tac ttt															8433
Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr Met Gly Ile Tyr Phe															
105 110 115															
gca aca cca gaa tgg gta gca ctc aat ggg cac cga ggg cca agc cca															8481
Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His Arg Gly Pro Ser Pro															
120 125 130															
ggc cag gta aag tac tgg cag aac aaa cga gaa ata ccg gac cca aac															8529
Gly Gln Val Lys Tyr Trp Gln Asn Lys Arg Glu Ile Pro Asp Pro Asn															
135 140 145															
gag gac tat cta gac tac gtg cat gca gag aag agc cgg ttg gca tca															8577
Glu Asp Tyr Leu Asp Tyr Val His Ala Glu Lys Ser Arg Leu Ala Ser															
150 155 160															
gaa gaa caa atc cta agg gca gct acg tcg atc tac ggg gct cca gga															8625
Glu Glu Gln Ile Leu Arg Ala Ala Thr Ser Ile Tyr Gly Ala Pro Gly															
165 170 175 180															
cag gca gag cca ccc caa gct ttc ata gac gaa gtt gcc aaa gtc tat															8673
Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu Val Ala Lys Val Tyr															
185 190 195															
gaa atc aac cat gga cgt ggc cca aac caa gaa cag atg aaa gat ctg															8721
Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu Gln Met Lys Asp Leu															
200 205 210															
ctc ttg act gcg atg gag atg aag cat cgc aat ccc agg cgg gct cta															8769
Leu Leu Thr Ala Met Glu Met Lys His Arg Asn Pro Arg Arg Ala Leu															
215 220 225															



cca	aag	ccc	aag	cca	aaa	ccc	aat	gct	cca	aca	cag	aga	ccc	cct	ggt	8817
Pro	Lys	Pro	Lys	Pro	Lys	Pro	Asn	Ala	Pro	Thr	Gln	Arg	Pro	Pro	Gly	
	230					235					240					
cgg	ctg	ggc	cgc	tgg	atc	agg	acc	gtc	tct	gat	gag	gac	ctt	gag	gga	8865
Arg	Leu	Gly	Arg	Trp	Ile	Arg	Thr	Val	Ser	Asp	Glu	Asp	Leu	Glu	Gly	
245					250					255					260	
tcc	atc	gcc	acc	atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	8913
Ser	Ile	Ala	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
				265					270					275		
gtg	ccc	atc	ctg	gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	8961
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			280					285					290			
agc	gtg	tcc	ggc	gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	9009
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		295					300					305				
ctg	aag	ttc	atc	tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	9057
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	310					315					320					
ctc	gtg	acc	acc	ctg	acc	tac	ggc	gtg	cag	tgc	ttc	agc	cgc	tac	ccc	9105
Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
325					330					335					340	
gac	cac	atg	aag	cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	9153
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				345					350					355		
tac	gtc	cag	gag	cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	9201
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			360					365					370			
acc	cgc	gcc	gag	gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	9249
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		375					380					385				
gag	ctg	aag	ggc	atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	9297
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	390					395					400					
aag	ctg	gag	tac	aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	9345
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
405					410					415					420	
aag	cag	aag	aac	ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	9393
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				425					430					435		
gag	gac	ggc	agc	gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	9441
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			440					445					450			
atc	ggc	gac	ggc	ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	acc	9489
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		455					460					465				

cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc 9537  
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
470 475 480

ctg	ctg	gag	ttc	gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	gag	9585
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	
485					490					495					500	

ctg tac aag taa agc 9600  
Leu Tyr Lys

<210>	10
<211>	503
<212>	PRT
<213>	Artificial sequence

<220>  
<223> pVP2-VP3-GFP protein

<400>	10														
Met	Ala	Ala	Ser	Glu	Phe	Lys	Glu	Thr	Pro	Glu	Leu	Glu	Ser	Ala	Val
1				5					10					15	
Arg	Ala	Met	Glu	Ala	Ala	Ala	Asn	Val	Asp	Pro	Leu	Phe	Gln	Ser	Ala
			20					25					30		
Leu	Ser	Val	Phe	Met	Trp	Leu	Glu	Glu	Asn	Gly	Ile	Val	Thr	Asp	Met
		35					40					45			
Ala	Asn	Phe	Ala	Leu	Ser	Asp	Pro	Asn	Ala	His	Arg	Met	Arg	Asn	Phe
	50					55					60				
Leu	Ala	Asn	Ala	Pro	Gln	Ala	Gly	Ser	Lys	Ser	Gln	Arg	Ala	Lys	Tyr
65					70					75					80
Gly	Thr	Ala	Gly	Tyr	Gly	Val	Glu	Ala	Arg	Gly	Pro	Thr	Pro	Glu	Glu
				85					90					95	
Ala	Gln	Arg	Glu	Lys	Asp	Thr	Arg	Ile	Ser	Lys	Lys	Met	Glu	Thr	Met
			100					105					110		
Gly	Ile	Tyr	Phe	Ala	Thr	Pro	Glu	Trp	Val	Ala	Leu	Asn	Gly	His	Arg
		115					120					125			
Gly	Pro	Ser	Pro	Gly	Gln	Val	Lys	Tyr	Trp	Gln	Asn	Lys	Arg	Glu	Ile
	130					135					140				
Pro	Asp	Pro	Asn	Glu	Asp	Tyr	Leu	Asp	Tyr	Val	His	Ala	Glu	Lys	Ser
145					150					155					160
Arg	Leu	Ala	Ser	Glu	Glu	Gln	Ile	Leu	Arg	Ala	Ala	Thr	Ser	Ile	Tyr
				165					170					175	
Gly	Ala	Pro	Gly	Gln	Ala	Glu	Pro	Pro	Gln	Ala	Phe	Ile	Asp	Glu	Val
			180					185					190		
Ala	Lys	Val	Tyr	Glu	Ile	Asn	His	Gly	Arg	Gly	Pro	Asn	Gln	Glu	Gln
		195					200					205			

Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn Pro  
 210 215 220  
 Arg Arg Ala Leu Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Thr Gln  
 225 230 235 240  
 Arg Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr Val Ser Asp Glu  
 245 250 255  
 Asp Leu Glu Gly Ser Ile Ala Thr Met Val Ser Lys Gly Glu Glu Leu  
 260 265 270  
 Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn  
 275 280 285  
 Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr  
 290 295 300  
 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
 305 310 315 320  
 Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe  
 325 330 335  
 Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala  
 340 345 350  
 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 355 360 365  
 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 370 375 380  
 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 385 390 395 400  
 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
 405 410 415  
 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
 420 425 430  
 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
 435 440 445  
 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 450 455 460  
 Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
 465 470 475 480  
 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
 485 490 495  
 Gly Met Asp Glu Leu Tyr Lys  
 500